STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	/o/8/2,238c
Source:	1FW16
Date Processed by STIC:	1/17/06
·	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
 Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/8/2, 238C
ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
lWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.
4_ V_Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
I0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING DATE: 01/17/2006
PATENT APPLICATION: US/10/812,238C TIME: 15:30:18

Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

```
3 <110> APPLICANT: Wary, Kishore, K.
              Humtsoe, Joseph O.
      6 <120> TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
              and Type I Collagen Inducible Protein (VCIP)
                                                                Sel Jens 2 and 4
on Evan Summary
Does Not Comply Sheet
Corrected Diskette Needed
      9 <130> FILE REFERENCE: D6563
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/812,238C
     12 <141> CURRENT FILING DATE: 2004-03-29
     14 <150> PRIOR APPLICATION NUMBER: US 60/458,164
     15 <151> PRIOR FILING DATE: 2003-03-27
     17 <160> NUMBER OF SEQ ID NOS: 42
     20 <210> SEQ ID NO: 1
     21 <211> LENGTH: 15
                                                                  pp2,6-8
     22 <212> TYPE: PRT
     23 <213> ORGANISM: Unknown
     25 <220> FEATURE:
     26 <221> NAME/KEY: CHAIN
     27 <223> OTHER INFORMATION: peptide used to raise anti-VCIP-cyto-C16
              antibody
     30 <400> SEQUENCE: 1
     31 Leu Ser Pro Val Asp Ile Ile Asp Arg Asn Asn His His Asn Met
     32
     35 <210> SEQ ID NO: 2
     36 <211> LENGTH: 20
     37 <212> TYPE: PRT
     38 <213> ORGANISM: Unknown
     40 <220> FEATURE:
     41 <221> NAME/KEY: CHAIN
     42 <223> OTHER INFORMATION: peptide used to raise anti-VCIP-RGD antibody
     44 <400> SEQUENCE: 2
     45 Glu Gly Tyr Ile Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys
                                               10
     47 Val Gln Glu Ala Arg
     48.
     51 <210> SEQ ID NO: 3
    52 <211> LENGTH: 33
     53 <212> TYPE: DNA
     54 <213> ORGANISM: Artificial Sequence
     56 <220> FEATURE:
    57 <221> NAME/KEY: primer_bind
    58 <223> OTHER INFORMATION: forward primer for VCIP
    60 <400> SEQUENCE: 3
    61 ggaggatccc tcgcgccgca gccagcgcca tgc
    64 <210> SEQ ID NO: 4
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Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

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65 <211> LENGTH: 25
66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <221> NAME/KEY: primer bind
71 <223> OTHER INFORMATION: reverse primer for VCIP
73 <400> SEQUENCE: 4
74 qtggcaccta catcatgttg tggtg
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 22
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <221> NAME/KEY: primer_bind
84 <223> OTHER INFORMATION: forward primer for human uPAR
86 <400> SEQUENCE: 5
87 cttcctgaaa tgcgtcaaca cc
                                22
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 22
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <221> NAME/KEY: primer_bind
97 <223> OTHER INFORMATION: reverse primer for human uPAR
99 <400> SEQUENCE: 6
100 tcatagctgg gaaaactgag gc
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 22
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
                                                              see p.6 for ever
109 <221> NAME/KEY: primer bind
110 <223> OTHER INFORMATION: forward primer for ?-actin
112 <400> SEQUENCE: 7
113 ggctgtgcta tccctgtacg cc
                                 22
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 22
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <221> NAME/KEY: primer_bind
123 <223> OTHER INFORMATION: reverse primer for ?-actin
125 <400> SEQUENCE: 8
126 gggcagtgat ctccttctgc at
129 <210> SEQ ID NO: 9
130 <211> LENGTH: 23
131 <212> TYPE: DNA
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134 <220> FEATURE:

132 <213> ORGANISM: Artificial Sequence

Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

135 <221> NAME/KEY: primer bind 136 <223> OTHER INFORMATION: forward primer for GAPDH 138 <400> SEQUENCE: 9 139 ggtctcctct gacttcaaca gcg 23 142 <210> SEQ ID NO: 10 143 <211> LENGTH: 24 144 <212> TYPE: DNA 145 <213> ORGANISM: Artificial Sequence 147 <220> FEATURE: 148 <221> NAME/KEY: primer bind 149 <223> OTHER INFORMATION: reverse primer for GAPDH 151 <400> SEQUENCE: 10 152 ggtactttat tgatggtaca tgac 24 155 <210> SEQ ID NO: 11 156 <211> LENGTH: 6 157 <212> TYPE: PRT 158 <213> ORGANISM: Unknown 160 <220> FEATURE: 161 <221> NAME/KEY: CHAIN 162 <223> OTHER INFORMATION: a peptide containing RGD sequence 164 <400> SEQUENCE: 11 165 Gly Arg Gly Asp Ser Pro 166 169 <210> SEQ ID NO: 12 170 <211> LENGTH: 9 171 <212> TYPE: PRT 172 <213> ORGANISM: Unknown 174 <220> FEATURE: 175 <221> NAME/KEY: CHAIN 176 <223> OTHER INFORMATION: HA-tag 178 <400> SEQUENCE: 12 179 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala 180 183 <210> SEQ ID NO: 13 184 <211> LENGTH: 311 185 <212> TYPE: PRT 186 <213> ORGANISM: Unknown 188 <220> FEATURE: 189 <221> NAME/KEY: CHAIN 190 <223> OTHER INFORMATION: human VCIP 192 <400> SEQUENCE: 13 193 Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys 10 15 195 Asn Gly Gly Ser Pro Ala Leu Asn Asn Pro Arg Arg Ser Gly 196 20 197 Ser Lys Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe 198 40 199 Met Ala Gly Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys 200 55

Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

```
201 Pro Tyr His Arg Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr
202
                                                               75
203 Pro Leu Lys Thr Gly Glu Thr Ile Asn Asp Ala Val Leu Cys Ala
204
                     80
                                          85
                                                               90
205 Val Gly Ile Val Ile Ala Ile Leu Ala Ile Ile Thr Gly Glu Phe
206
                     95
                                         100
207 Tyr Arg Ile Tyr Tyr Leu Lys Lys Ser Arg Ser Thr Ile Gln Asn
208
                    110
                                         115
209 Pro Tyr Val Ala Ala Leu Tyr Lys Gln Val Gly Cys Phe Leu Phe
210
                    125
                                         130
211 Gly Cys Ala Ile Ser Gln Ser Phe Thr Asp Ile Ala Lys Val Ser
213 Ile Gly Arg Leu Arg Pro His Phe Leu Ser Val Cys Asn Pro Asp
214
                    155
                                                              165
215 Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile Gln Asn Tyr Arg
216
                    170
                                         175
                                                              180
217 Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg Lys Ser Phe
218
                    185
                                         190
219 Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu Tyr Leu
                    200
                                         205
                                                              210
221 Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg Leu
222
                    215
                                         220
                                                              225
223 Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr
                    230
224
                                         235
225 Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp
                    245
                                         250
227 Val Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile
228
                    260
                                         265
                                                              270
229 Val Phe Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser
230
231 Leu Pro Ala Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp
232
                    290
                                         295
                                                              300
233 Ile Ile Asp Arg Asn Asn His His Asn Met Met
234
237 <210> SEQ ID NO: 14
238 <211> LENGTH: 18
239 <212> TYPE: PRT
240 <213> ORGANISM: Unknown
242 <220> FEATURE:
243 <221> NAME/KEY: CHAIN
244 <223> OTHER INFORMATION: lipid phosphatase domain of human VCIP
246 <400> SEQUENCE: 14
247 Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu
248
249 Ser Val Cys
252 <210> SEQ ID NO: 15
253 <211> LENGTH: 18
254 <212> TYPE: PRT
255 <213> ORGANISM: Unknown
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Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

```
257 <220> FEATURE:
258 <221> NAME/KEY: CHAIN
259 <223> OTHER INFORMATION: a rat peptide containing lipid
260
          phosphatase domain
262 <400> SEQUENCE: 15
263 Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu
264
                     5
                                          10
265 Ala Val Cys
268 <210> SEQ ID NO: 16
269 <211> LENGTH: 18
270 <212> TYPE: PRT
271 <213> ORGANISM: Unknown
273 <220> FEATURE:
274 <221> NAME/KEY: CHAIN
275 <223> OTHER INFORMATION: a mouse peptide containing lipid
          phosphatase domain
278 <400> SEQUENCE: 16
279 Asp Ile Ala Lys Tyr Thr Ile Gly Ser Leu Arg Pro His Phe Leu
280
                     5
281 Ala Ile Cys
284 <210> SEQ ID NO: 17
285 <211> LENGTH: 18
286 <212> TYPE: PRT
287 <213> ORGANISM: Unknown
289 <220> FEATURE:
290 <221> NAME/KEY: CHAIN
291 <223> OTHER INFORMATION: a human peptide containing lipid
          phosphatase domain
294 <400> SEQUENCE: 17
295 Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Arg Pro Asn Phe Leu
296
297 Ala Val Cys
300 <210> SEQ ID NO: 18
301 <211> LENGTH: 18
302 <212> TYPE: PRT
303 <213> ORGANISM: Unknown
305 <220> FEATURE:
306 <221> NAME/KEY: CHAIN
307 <223> OTHER INFORMATION: a Drosophila peptide containing lipid
          phosphatase domain
310 <400> SEQUENCE: 18
311 Asn Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Tyr
312
                     5
                                                              15
313 Thr Leu Cys
316 <210> SEQ ID NO: 19
317 <211> LENGTH: 18
318 <212> TYPE: PRT
319 <213> ORGANISM: C. elegans
321 <220> FEATURE:
```

<210>	7
<211>	22
<212>	DNA
<213>	Artificial Sequence
<220>	do not use scientific
<221>	primer_bind do not use scientific symbols
<223>	_ / /
1220	forward primer for β actin of freign occurt
<400>	- 0 0 0 0
	tecetgtacg cc 22 / marks. They
	carrot
	le proused.
	Please spell the
	und
	This type of
-	enor oppears in subsequent sequences.
	seguest seguest
	in subsequent

10/8/2,238c 7

<210> 40 <211> 12 <212> PRT <213> Artificial Sequence ? This is a pertide of sequence. <220> <221> anti-sense primer for mouse GAPDH <223> <400> 40 Ser Arg Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Asp 5 10 I had is not a sufficient explanation's for Xaa!s. See P. 8 for evor 22217 levi is not used to Iglan n's or Xaa's



VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/812,238C

DATE: 01/17/2006 TIME: 15:30:19

Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:38; Xaa Pos. 2,3,4,5,6,7

Seq#:40; Xaa Pos. 3,4,5,6,7,9,10,11

VERIFICATION SUMMARY

DATE: 01/17/2006 PATENT APPLICATION: US/10/812,238C TIME: 15:30:19

Input Set : N:\SMITH\PTO.TAS16.txt

Output Set: N:\CRF4\01172006\J812238C.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0

L:613 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:40

L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0